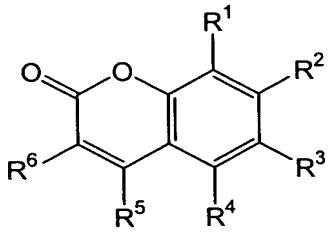
WHAT IS CLAIMED IS:

1. A material having a fluorogenic moiety linked to a solid support, said material having the structure:



wherein:

R^1, R^2, R^3, R^4, R^5 and R^6 are members independently selected from the group consisting of H, halogen, $-NO_2$, -CN, $-C(O)_mR^7$, $-C(O)NR^8R^9$, $-S(O)_tR^{10}$, $-SO_2NR^{11}R^{12}$, $-OR^{13}$, substituted or unsubstituted alkyl, $-R^{14}$-*SS*, and $-NHR^{15}$ with the proviso that at least one of R^1, R^2, R^3, R^4, R^5 and R^6 is $-R^{14}$-*SS* and at least one of R^1, R^2, R^3, R^4, R^5 and R^6 is $-NHR^{15}$,

wherein:

R^7, R^8, R^9, R^{10}, R^{11}, R^{12} and R^{13} are members independently selected from the group consisting of H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl;

R^{14} is a linking group adjoining said fluorogenic moiety and said solid support;

R^{15} is a member selected from the group consisting of amine protecting groups, -C(O)-AA and -C(O)-P:

wherein:

P is a peptide sequence;

AA is an amino acid residue;

m is a member selected from the group consisting of the integers 1 and 2;

t is a member selected from the group consisting of the integers from 0 to 2; and

SS is a solid support.

2. The material according to claim **1**, wherein said linking group is a member selected from the group consisting of substituted or unsubstituted alkyl, substituted or unsubstituted heteroalkyl and substituted or unsubstituted aryl;

3. The material according to claim **1**, wherein P is a peptide sequence comprising the structure:

$$-C(O)-AA^1-AA^2-(AA^i)_{J-2}$$

wherein,

AA^1-AA^2-$(AA^i)_{J-2}$ is a peptide sequence, wherein each of AA^1 through AA^i is an amino acid residue which is a member independently selected from the group of natural amino acid residues, unnatural amino acid residues and modified amino acid residues;

J denotes the number of amino acid residues forming said peptide sequence and is a member selected from the group consisting of the numbers from 2 to 10, such that *J*-2 is the number of amino acid residues in the peptide sequence exclusive of AA^1-AA^2; and

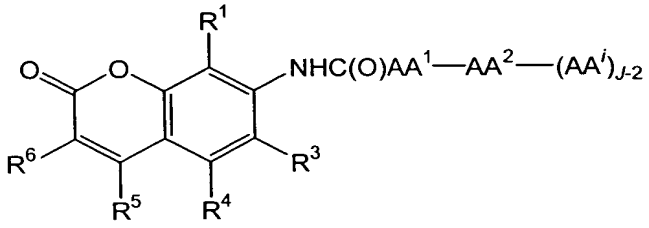
i denotes the position of said amino acid residue relevant to AA^1 and when *J* is greater than 2, *i* is a member selected from the group consisting of the numbers from 3 to 10.

4. The material according to claim **1**, wherein R^{15} has the structure:

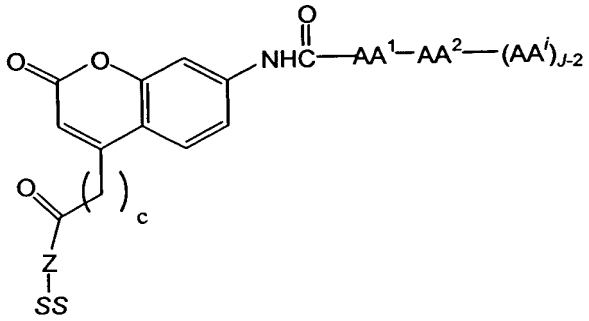
$$-C(O)-AA;$$ and

AA is an amino acid residue selected from the group consisting of natural amino acids, unnatural amino acids and modified amino acids.

5. The material according to claim **1**, having the structure:



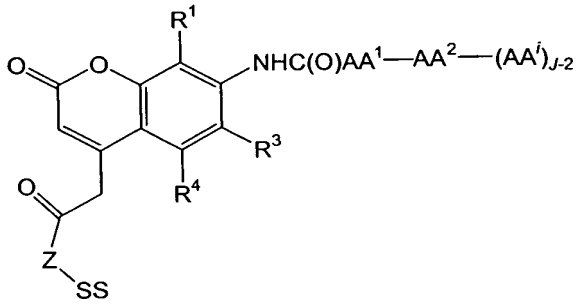
6. The material according to claim **5**, having the structure:



wherein, Z is a member selected from the group consisting of –O-, and –-NR^{16}-; and

c is a member selected from the integers from 0 to 6.

7. A material according to claim **6**, having the structure:



8. A method of assaying for the presence of an enzymatically active protease in a sample, said method comprising:

(a) contacting said sample with a material according to claim **3** in such a manner whereby said fluorogenic moiety is released from said peptide sequence upon action of said protease, thereby producing a fluorescent moiety; and

(b) observing whether said sample undergoes a detectable change in fluorescence, said detectable change being an indication of the presence of said enzymatically active protease in said sample.

9. The method according to claim **8**, wherein said protease is a member selected from the group consisting of aspartic protease, cysteine protease, metalloprotease and serine protease.

10. The method according to claim **8**, wherein said protease is a protease of a microorganism.

11. The method according to claim **10**, wherein said microorganism is a member selected from the group consisting of bacteria, fungi, yeast, viruses, and protozoa.

12. The method according to claim **8**, wherein said sample is a clinical sample from a subject.

13. The method according to claim **8**, further comprising (c) quantifying said fluorescent moiety, thereby quantifying said protease.

14. A method of assaying for the presence of a selected microorganism in a sample by probing the sequence specificity of peptide cleavage by a protease of said microorganism, said method comprising:

(a) contacting a sample suspected of containing said selected microorganism with a material according to claim **3**, wherein said peptide comprises a sequence that is selectively cleaved by said protease of said selected microorganism, thereby releasing the fluorogenic moiety from the peptide sequence;

(b) detecting the cleavage by detecting fluorescence arising from a fluorescent moiety produced by cleavage of said fluorogenic moiety from said peptide sequence, thereby confirming said presence of said selected microorganism in said sample.

15. The method according to claim **14**, further comprising (c) quantifying said fluorescence, thereby quantifying said protease of said microorganism.

16. A fluorogenic peptide comprising a fluorogenic moiety covalently bound to a peptide sequence, said peptide having the structure:

R-P

wherein:

P is a peptide sequence having the structure:

$$-C(O)-AA^{1}-AA^{2}-(AA^{i})_{J-2}$$

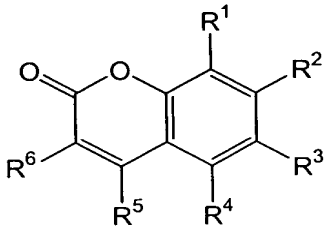
wherein:

each of AA^1 through AA^i is an amino acid residue which is a member independently selected from the group of natural amino acid residues, unnatural amino acid residues and modified amino acid residues;

J denotes the number of amino acid residues forming said peptide sequence and is a member selected from the group consisting of the numbers from 2 to 10, such that *J*-2 is the number of amino acid residues in the peptide sequence exclusive of AA^1-AA^2;

i denotes the position of said amino acid residue in sequence relative to AA^1 and when *J* is greater than 2, *i* is a member selected from the group consisting of the numbers from 3 to 10; and

R is a fluorogenic moiety having the structure:



wherein:

R^1, R^2, R^3, R^4, R^5 and R^6 are members independently selected from the group consisting of H, halogen, $-NO_2$, -CN, $-C(O)_mR^6$, $-C(O)NR^7R^8$, $-S(O)_tR^9$, $-SO_2NR^{10}R^{11}$, $-OR^{12}$, substituted or unsubstituted alkyl, -NHC(O)-P, and $-R^{20}$-Y, with the proviso that at least one of R^1, R^2, R^3, R^4, R^5 and R^6 is $-R^{20}$-Y and at least one of R^1, R^2, R^3, R^4, R^5 and R^6 is -NHC(O)-P,

wherein:

R^6, R^7, R^8, R^9, R^{10}, R^{11} and R^{12} are members independently selected from the group consisting of H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl;

R^{20} is either present or absent and is a member selected from the group consisting of substituted or unsubstituted alkyl and substituted or unsubstituted heteroalkyl;

Y is a member selected from the group consisting of organic functional groups and methyl;

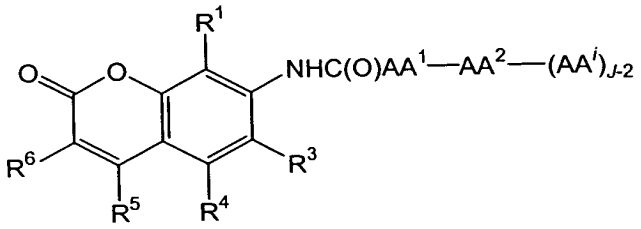
m is a member selected from the group consisting of the integers 1 and 2; and

t is a member selected from the group consisting of the integers from 0 to 2.

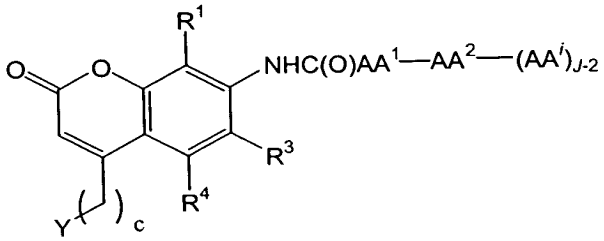
17. The fluorogenic peptide according to claim **16**, wherein said organic functional group is a member selected from the group consisting of $-COOR^{17}$, $CONR^{17}R^{21}$, $-C(O)R^{17}R^{21}$, $-OR^{17}$, $-SR^{17}$, $-C(O)SR^{17}$ and $-NR^{17}R^{21}$

wherein, R^{17} and R^{21} are members independently selected from H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl.

18. A fluorogenic peptide according to claim **16**, having the structure:



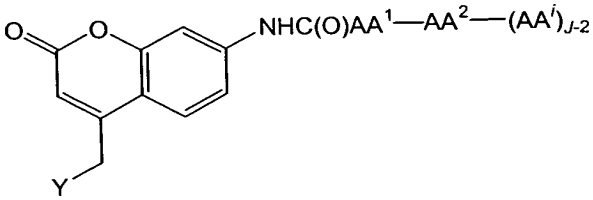
19. A fluorogenic peptide according to claim **18**, having the structure:



wherein:

c is a member selected from the group consisting of the integers from 0 to 6.

20. A fluorogenic peptide according to claim **19**, having the structure:



21. The fluorogenic peptide according to claim **16**, wherein said peptide sequence comprises a peptide bond that is cleaved by a protease releasing said fluorogenic moiety from said peptide sequence, thereby producing a fluorescent moiety and a peptide moiety.

22. The fluorogenic peptide according to claim **21**, wherein said peptide bond is formed between a carboxyl of the carboxy-terminus amino acid residue and an amine group of said fluorogenic moiety.

23. A method of assaying for the presence of an enzymatically active protease in a sample, said method comprising:

(a) contacting a sample suspected of containing said protease with a peptide according to claim **16** in such a manner whereby said fluorogenic moiety is released from said peptide sequence upon action of said protease, thereby producing a fluorescent moiety; and

(b) observing whether said sample undergoes a detectable change in fluorescence, said detectable change being an indication of the presence of said enzymatically active protease in said sample.

24. The method according to claim **23**, wherein said protease is a member selected from the group consisting of aspartic protease, cysteine protease, metalloprotease and serine protease.

25. The method according to claim **23**, wherein said protease is a protease of a microorganism.

26. The method according to claim **25**, wherein said microorganism is a member selected from the group consisting of bacteria, fungi, yeast, viruses, and protozoa.

27. The method according to claim **23**, wherein said sample is a clinical sample from a subject.

28. The method according to claim **27**, wherein said subject is a human.

29. The method according to claim **23**, further comprising (c) quantifying said fluorescent moiety, thereby quantifying said protease.

30. A method of assaying for the presence of a selected microorganism in a sample by probing the sequence specificity of peptide cleavage by a protease of said microorganism, said method comprising:

(a) contacting a sample suspected of containing said selected microorganism with a material according to claim **16**, wherein said peptide comprises a sequence that is selectively cleaved by a protease of a selected microorganism, thereby releasing said fluorogenic moiety from said peptide sequence;

(b) detecting said cleavage by detecting fluorescence arising from a fluorescent moiety produced by cleavage of said fluorogenic moiety from said peptide sequence, thereby confirming said presence of said selected microorganism in said sample.

31. The method according to claim **30**, further comprising (c) quantifying said fluorescence, thereby quantifying said protease of said microorganism.

32. A library of fluorogenic peptides comprising at least a first peptide having a first peptide sequence covalently attached to a first fluorogenic moiety and a second peptide having a second peptide sequence covalently attached to a second fluorogenic moiety, said first peptide and said second peptide having the structure:

R-P

wherein:

for each of said first peptide and said second peptide, P is independently selected from peptide sequences having the structure:

$$-C(O)-AA^{1}-AA^{2}-(AA^{i})_{J-2}$$

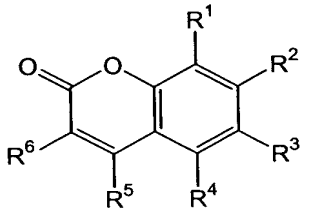
wherein:

each of AA^{1} through AA^{i} is an amino acid residue which is a member independently selected from the group consisting of natural amino acid residues, unnatural amino acid residues and modified amino acid residues;.

each J is independently selected and denotes the number of amino acid residues forming said first peptide sequence and said second peptide sequence and is a member selected from the group consisting of the numbers from 2 to 10;

each i is independently selected and denotes the position of said amino acid residue relative to AA^1 and when J is greater than 2, i is a member selected from the group consisting of the numbers from 3 to 10; and

for each of said first peptide and said second peptide R is independently selected from fluorogenic moieties having the structure:



wherein:

R^1, R^2, R^3, R^4, R^5, and R^6 are members independently selected from the group consisting of H, halogen, $-NO_2$, -CN, $-C(O)_mR^7$, $-C(O)NR^8R^9$, $-S(O)_tR^{10}$, $-SO_2NR^{11}R^{12}$, $-OR^{13}$, substituted or unsubstituted alkyl, -NH-C(O)-P, R^{20}-Y and $-R^{14}$-*SS*, with the proviso that for each peptide at least one of R^1, R^2, R^3, R^4 and R^5 is a member independently selected from $-R^{14}$-*SS* and R^{20}-Y and at least one of R^1, R^2, R^3, R^4, R^5, and R^6 is -NH-C(O)-P,

wherein:

R^7, R^8, R^9, R^{10}, R^{11}, R^{12} and R^{13} are members independently selected from the group consisting of H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl;

R^{14} is a linking group adjoining said fluorogenic moiety and the solid support;

R^{20} is either present or absent and is a member selected from the group consisting of substituted or unsubstituted alkyl and substituted or unsubstituted heteroalkyl;

Y is a member selected from the group consisting of organic functional groups and methyl;

m is a member selected from the group consisting of the integers from 1 to 2;

t is a member selected from the group consisting of the integers from 0 to 2;

Y is a member selected from the group consisting of $-COOR^{17}$, $CONHR^{17}$, $-C(O)R^{17}$, $-OR^{17}$, $-SR^{17}$, and NHR^{17};

R^{17} is a member selected from the group consisting of H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl; and

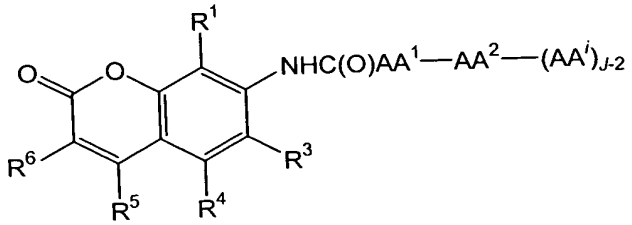
SS is a solid support.

33. The library according to claim **32**, wherein said linking group is a member selected from the group consisting of substituted or unsubstituted alkyl and substituted or unsubstituted heteroalkyl

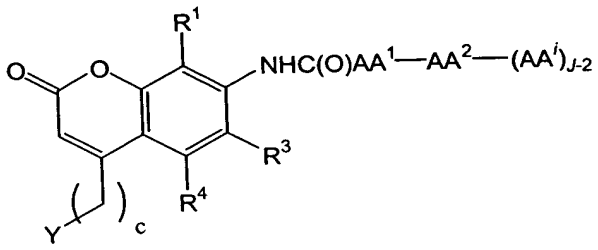
34. The library according to claim **32**, wherein said organic functional group is a member selected from the group consisting of $-COOR^{17}$, $CONR^{17}R^{21}$, $-C(O)R^{17}R^{21}$, $-OR^{17}$, $-SR^{17}$, $-C(O)SR^{17}$, and $-NR^{17}R^{21}$

wherein, R^{17} and R^{21} are members independently selected from H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl.

35. The library of fluorogenic peptides according to claim **32**, wherein R-P has the structure:



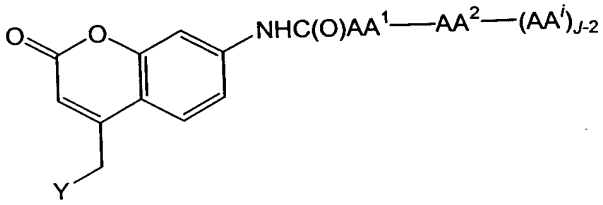
36. A library of fluorogenic peptides according to claim **35**, wherein R-P has the structure:



wherein,

c is a member selected from the group consisting of the numbers from 0 to 6.

37. A library of fluorogenic peptides according to claim **36**, wherein R-P has the structure:



38. The library according to claim **32**, wherein said fluorogenic moiety of said first peptide and said fluorogenic moiety of said second peptide are different fluorogenic moieties.

39. The library according to claim **32**, wherein said first peptide sequence and said second peptide sequence are identical.

40. The library according to claim **32**, wherein said first peptide sequence and said second peptide sequence are different.

41. The library according to claim **40**, wherein an amino acid residue selected from the group consisting of AA^1, AA^2, AA^i and combinations thereof of said first peptide is a different amino acid residue than an amino acid residue at a corresponding position relative to AA^1 of said second peptide.

42. The library according to claim **32**, wherein AA^1 of said first peptide sequence and AA^1 of said second peptide sequence are identical amino acid residues.

43. The library according to claim **32**, wherein AA^1 of said first peptide sequence and AA^1 of said second peptide sequence are different amino acid residues.

44. The library according to claim **32**, wherein AA^2 of said first peptide sequence and AA^2 of said second peptide sequence are identical amino acid residues.

45. The library according to claim **32**, wherein AA^2 of said first peptide sequence and AA^2 of said second peptide sequence are different amino acid residues.

46. The library according to claim **32**, wherein AA^i of said first peptide sequence and AA^i of said second peptide sequence are identical amino acid residues.

47. The library according to claim **32**, wherein AA^i of said first peptide sequence and AA^i of said second peptide sequence are different amino acid residues.

48. The library according to claim **42**, comprising at least six peptides having different peptide sequences, wherein AA^1 is a different amino acid residue in each of said different peptide sequences.

49. The library according to claim **48**, comprising at least twelve peptides having different peptide sequences wherein AA^1 is a different amino acid residue in each of said different peptide sequences.

50. The library according to claim **49**, comprising at least twenty peptides having different peptide sequences wherein AA^1 is a different amino acid residue in each of said different peptide sequences.

51. The library according to claim **32**, wherein AA^1 is a member selected from the group consisting of Lys, Arg, Leu and combinations thereof.

52. The library according to claim **32**, wherein J is a member selected from the numbers from 4 to 8.

53. The library of peptides according to claim **32**, wherein at least one of said first peptide and said second peptide is cleavable by a protease into a fluorescent moiety and the peptide sequence.

54. The library according to claim **32**, comprising at least 10 peptides, wherein each of the peptide sequences is a different peptide sequence.

55. The library according to claim **54**, comprising at least 100 peptides, wherein each of the peptide sequences is a different peptide sequence.

56. The library according to claim **55**, comprising at least 1,000 peptides, wherein each of the peptide sequences is a different peptide sequence.

57. The library according to claim **56**, comprising at least 10,000 peptides, wherein each of the peptide sequences is a different peptide sequence.

58. The library according to claim **57**, comprising at least 100,000 peptides, wherein each of the peptide sequences is a different peptide sequence.

59. The library according to claim **58** comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence.

60. The library according to claim **32**, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate.

61. A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising:

(a) contacting said protease with a library of peptides according to claim **32** in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;

(b) detecting said fluorescent moiety;

(c) determining the sequence of said peptide sequence, thereby determining said peptide sequence specificity profile of said protease.

62. The method according to claim 61, further comprising (d) quantifying said fluorescent moiety, thereby quantifying said protease.

63. A database comprising at least one set of peptide sequence specificity data for a protease determined using a library according to claim 32.

64. The database according to claim 63, wherein said database is an electronic database.

65. The database according to claim 64, wherein said database is distributed on a wide area network.

66. A database comprising at least one set of peptide sequence specificity data for a protease determined using a method according to claim 61.

67. The database according to claim 63, wherein said database is an electronic database.

68. The database according to claim 64, wherein said database is distributed on a wide area network.

69. The method according to claim 61, wherein said protease is a member selected from the group consisting of aspartic protease, cysteine protease, and serine protease

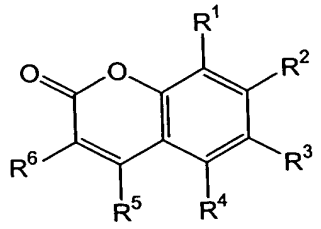
70. The method according to claim 61, wherein said protease is a protease of a microorganism.

71. The method according to claim 70, wherein said microorganism is a member selected from the group consisting of bacteria, fungi, yeast, viruses, and protozoa.

72. The method according to claim 61, further comprising (c) quantifying the fluorescent moiety, thereby quantifying said protease.

73. A method of preparing a fluorogenic peptide, said method comprising:

(a) providing a first conjugate comprising a fluorogenic moiety covalently bonded to a solid support, said conjugate having the structure:



wherein,

R^1, R^2, R^3, R^4, R^5 and R^6 are members independently selected from the group consisting of H, halogen, $-NO_2$, -CN, $-C(O)_mR^7$,$-C(O)NR^8R^9$, $-S(O)_tR^{10}$, $-SO_2NR^{11}R^{12}$, $-OR^{13}$ $-NR^{18}R^{19}$, and substituted or unsubstituted alkyl, with the proviso that at least one of R^1, R^2, R^3, R^4, R^5 and R^6 is $-NH_2$;

R^7, R^8, R^9, R^{10}, R^{11}, R^{12}, R^{13}, R^{18} and R^{19} are members independently selected from the group consisting of H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl;

m is a member selected from the group consisting of the numbers from 1 to 2;

t is a member selected from the group consisting of the numbers from 0 to 2;

R^5 and R^6 are members independently selected from the group consisting of H and $-R^{14}$-C(O)NH-*SS*, wherein at least one of R^5 and R^6 is $-R^{14}$-C(O)NH-*SS*;

R^{14} is a member selected from the group consisting of substituted or unsubstituted alkyl and substituted or unsubstituted heteroalkyl;

SS is a solid support;

(b) contacting said first conjugate with a first protected amino acid moiety (pAA^1) and an activating agent, thereby forming a peptide bond between a carboxyl group of pAA^1 and the aniline nitrogen of said first conjugate;

(c) deprotecting said pAA^1, thereby forming a second conjugate having a reactive AA^1 amine moiety;

(d) contacting said second conjugate with a second protected amino acid (pAA^2) and an activating agent, thereby forming a peptide bond between a carboxyl group of pAA2 and said reactive AA^1 amine moiety; and

(e) deprotecting said pAA^2, thereby forming a third conjugate having a reactive AA^2 amine moiety.

74. The method according to claim **73**, further comprising:

(f) contacting said third conjugate with a third protected amino acid (pAA^3) and an activating agent, thereby forming a peptide bond between a carboxyl group of pAA^3 and said reactive AA^2 amine moiety; and

(e) deprotecting said pAA^3, thereby forming a fourth conjugate having a reactive AA^3 amine moiety.

75. The method according to claim **73**, further comprising between steps (b) and (c) capping aniline amine groups that have not reacted with pAA^1.

76. The method according to claim **75**, wherein said capping utilizes a mixture comprising an active ester of a carboxylic acid.

77. The method according to claim **78**, wherein said active ester is the nitrotriazole ester of acetic acid.

78. The method according to claim **74**, wherein a member selected from the group consisting of pAA^1, pAA^2, pAA^3 and combinations thereof comprises a mixture of protected amino acids differing in the identity of the amino acid portion of the protected amino acids.

79. The method according to claim **78**, wherein said mixture comprises at least 2 unique amino acids.

80. The method according to claim **79**, wherein said mixture comprises at least 6 unique amino acids.

81. The method according to claim **80**, wherein said mixture comprises at least 12 unique amino acids.

82. The method according to claim **81**, wherein said mixture comprises at least 20 unique amino acids.

83. The method according to claim **78**, wherein said mixture is an isokinetic mixture.